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RAW SEQUENCE LISTING

DATE: 11/27/2001

PATENT APPLICATION: US/09/922,600

TIME: 13:46:09

Input Set : A:\09922600.raw.txt

Output Set: N:\CRF3\11212001\I922600.raw

PS

1 <110> APPLICANT: Goodman, Corey
 2 Kid, Thomas
 3 Brose, Katja
 4 Tessier-Lavigne, Marc
 5 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
 6 <130> FILE REFERENCE: B98-031-3
 7 <140> CURRENT APPLICATION NUMBER: 09/922,600
 8 <141> CURRENT FILING DATE: 2001-08-03
 9 <150> PRIOR APPLICATION NUMBER: US/09/540,245
 10 <151> PRIOR FILING DATE: 2000-03-31
 11 <150> PRIOR APPLICATION NUMBER: 60/065,544
 12 <151> PRIOR FILING DATE: 1997-11-14
 13 <150> PRIOR APPLICATION NUMBER: 60/081,057
 14 <151> PRIOR FILING DATE: 1998-04-07
 15 <160> NUMBER OF SEQ ID NOS: 20
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 4758
 20 <212> TYPE: DNA
 21 <213> ORGANISM: human
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(4755)
 25 <400> SEQUENCE: 1

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27	Met Arg Gly Val Gly Trp Gln Met Leu Ser Leu Ser Leu Gly Leu Val	
28	1 5 10 15	
29	ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc	96
30	Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys	
31	20 25 30	
32	tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc	144
33	Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser	
34	35 40 45	
35	gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga	192
36	Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly	
37	50 55 60	
38	aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat	240
39	Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His	
40	65 70 75 80	
41	cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga	288
42	Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg	
43	85 90 95	
44	gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga	336
45	Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg	
46	100 105 110	
47	aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag	384
48	Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys	

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98      gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac      1200
99      Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His
100      385              390              395              400
101      aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc      1248
102      Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
103              405              410              415
104      aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc      1296
105      Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
106              420              425              430
107      cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat      1344
108      Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
109              435              440              445
110      ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc      1392
111      Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
112              450              455              460
113      cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc      1440
114      Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
115      465              470              475              480
116      cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc      1488
117      Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
118              485              490              495
119      ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca      1536
120      Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
121              500              505              510
122      gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc      1584
123      Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro
124              515              520              525
125      cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg      1632
126      Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu
127              530              535              540
128      gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac      1680
129      Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn
130      545              550              555              560
131      ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga      1728
132      Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Gly Ala Phe Glu Gly
133              565              570              575
134      gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat      1776
135      Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn
136              580              585              590
137      gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg      1824
138      Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met
139              595              600              605
140      ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga      1872
141      Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly
142              610              615              620
143      ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca      1920
144      Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr
145      625              630              635              640
146      gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac      1968

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147	Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn	
148		645 650 655
149	ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga	2016
150	Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly	
151		660 665 670
152	gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa	2064
153	Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln	
154		675 680 685
155	aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag	2112
156	Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln	
157		690 695 700
158	gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt	2160
159	Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu	
160		705 710 715 720
161	tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt	2208
162	Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys	
163		725 730 735
164	agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc	2256
165	Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val	
166		740 745 750
167	aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa	2304
168	Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu	
169		755 760 765
170	ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga	2352
171	Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg	
172		770 775 780
173	ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc	2400
174	Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu	
175		785 790 795 800
176	acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc	2448
177	Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr	
178		805 810 815
179	ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac	2496
180	Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp	
181		820 825 830
182	att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca	2544
183	Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser	
184		835 840 845
185	cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag	2592
186	His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln	
187		850 855 860
188	tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct	2640
189	Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala	
190		865 870 875 880
191	cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act	2688
192	Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr	
193		885 890 895
194	ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta	2736
195	Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu	

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196		900		905		910		
197	gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca							2784
198	Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr							
199		915		920		925		
200	tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt							2832
201	Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly							
202		930		935		940		
203	ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac							2880
204	Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn							
205		945		950		955		960
206	cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat							2928
207	Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp							
208		965		970		975		
209	gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa							2976
210	Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu							
211		980		985		990		
212	gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca							3024
213	Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr							
214		995		1000		1005		
215	tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat							3072
216	Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr							
217		1010		1015		1020		
218	aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg							3120
219	Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu							
220		1025		1030		1035		1040
221	aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc							3168
222	Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe							
223		1045		1050		1055		
224	aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat							3216
225	Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp							
226		1060		1065		1070		
227	ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca							3264
228	Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr							
229		1075		1080		1085		
230	gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc							3312
231	Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly							
232		1090		1095		1100		
233	ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc							3360
234	Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro							
235		1105		1110		1115		1120
236	tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata							3408
237	Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile							
238		1125		1130		1135		
239	aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt							3456
240	Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys							
241		1140		1145		1150		
242	gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag							3504
243	Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln							
244		1155		1160		1165		

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\09922600.raw.txt

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L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19